the invention. Isolated polyclonal or monoclonal antibodies that bind to peptides encoded by SEQ ID NOS: 1-327 are also encompassed by the invention.

[027] Further encompassed by this invention are methods for using the nucleic acid molecules of any one of SEQ ID NOS: 1-327 to obtain full length cDNA and genomic sequences of the corresponding genes, including cognate, homologous, or otherwise related genetic sequences, which hybridize to any of SEQ ID NOS: 1-327 under conditions of moderate or high stringency. Also provided by this invention are oligonucleotides derived from any one of SEQ ID NOS: 1-334 that can be used as probes and/or as primers in PCR, RT-PCR, and other assays to detect the presence or level of the nucleic acids of SEQ ID NOS: 1-334 and related molecules.

[028] The primers and other probes of the invention may be used to monitor and characterize the development of plant embryos, in particular, pine tree embryos. Characterization of embryonic gene expression provides means for correlating gene expression with current and potential plant phenotypes. Consequently, the present invention encompasses means for monitoring and adjusting growth conditions (see Figure 6), as well as means for selecting genetically superior embryonic clones for further propagation and expansion (see Figure 8). Thus, the present invention encompasses the use of DNA or RNA probes derived from the nucleic acid molecules of SEQ ID NOS: 1-334 in any form, e.g., in DNA arrays, and antibodies raised against polypeptides or peptide fragments encoded by SEQ ID NOS: 1-327, to determine relative or absolute levels of expression of the genes or proteins encoded by SEQ ID NOS: 1-327. In addition, these nucleic acid and antibody probes may be used for

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staging, monitoring, characterizing, or selecting plant embryos or embryo cultures, particularly pine tree embryos.

[029] The relational database of the present invention allows expression information pertaining to embryo stages to be viewed as sequence data generated in accordance with the present invention. The invention includes a database for storing a plurality of sequence records for which to correlate embryo stages to sequence records. The method further involves providing an interface which allows a user to select one or more expression categories contained within the database.

[030] The relational database is designed to include separate parts or cells for information storage. One cell or part may contain a gene expression database which contains nucleic acid molecules of SEQ ID NOS: 1-327. Other cells or parts may contain descriptive information pertaining to each nucleic acid molecules of SEQ ID NOS: 1-327, additional sequence data related to the gene expression database, protein encoded by nucleic acids disclosed herein, similarity values to known proteins of other systems, and to conditions under which expression data was obtained.

[031] The database system described in the present invention will allow identification or selection of particular genes of interest for further use with DNA arrays. Identification or selection of particular genes may include, for example, those related to patterns of expression, those identified with homology to known genes from other studies, and those sequences considered novel.

BRIEF DESCRIPTION OF THE DRAWINGS

[032] FIG. 1 depicts differential display of loblolly pine zygotic and somatic embryos at different stages of development.

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[033] FIG. 2 displays embryo gene expression observed by high-density array Southern hybridization.

[034] FIG. 3 provides a general schematic for gene regulation studies arising from the cDNA cloning of genes expressed in embryos.

[035] FIG. 4 depicts graphical representation of hybridization of 'dehydrin' and LPZ216 cDNA probes to total RNA isolated from zygotic embryos of loblolly pine.

[036] FIG. 5 displays ABA concentration of loblolly pine embryos.

[037] FIG. 6 shows schematic of gene study for improved somatic embryogenesis.

[038] FIG. 7 shows detection of gene expression by high-density array Southern hybridization for loblolly pine genotype 333 after 12 weeks on two maturation media.

[039] FIG. 8 depicts the application of embryogenic gene expression studies.

[040] FIG. 9 displays slot blots and expression levels for three embryogenesis-related genes.

FIG. 10 depicts clone LPS-097 sequence (LP2-3 differential display fragment.)

FIG. 11 displays a northern blot for the LP2-3 gene during stages 1-3.

FIG. 12 displays a slot blot of total RNA from somatic embryo tissue probed with an LP2-3-specific probe.

FIG. 13 displays a slot blot of total RNA from zygotic embryo tissue probed with an LP2-3-specific probe.

[041] FIG. 14 depicts the quantified expression of early zygotic embryos compared to early somatic embryos.

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